

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/070,277A

Source: 1FW16

Date Processed by STIC: 8/2/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 08/02/2005

PATENT APPLICATION: US/10/070,277A

TIME: 15:48:58

Input Set : N:\KEISHA\10070277A.txt

Output Set: N:\CRF4\08022005\J070277A.raw

```

3 <110> APPLICANT: Ehrhardt, Thomas
4     Lerchl, Jens
5     Nigel, Marc Stitt
6     Zenner, Rita
8 <120> TITLE OF INVENTION: Plant dihydroorotase
10 <130> FILE REFERENCE: 0050/50716
12 <140> CURRENT APPLICATION NUMBER: US 10/070,277A
13 <141> CURRENT FILING DATE: 2002-03-06
15 <150> PRIOR APPLICATION NUMBER: PCT/EP00/08581
16 <151> PRIOR FILING DATE: 2000-09-02
19 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: Microsoft Word 2003
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1271
26 <212> TYPE: DNA
27 <213> ORGANISM: Solanum tuberosum
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (9)..(1046)
33 <400> SEQUENCE: 1
35 ttgcaaaa atg gag ctc tca atc aca caa cct gat gat tgg cat ctt cat 50
36     Met Glu Leu Ser Ile Thr Gln Pro Asp Asp Trp His Leu His
37     1             5             10
39 ctc cgt gat ggt gat gtt ctt aag gca gtt gtc tct cac agt gca cat 98
40 Leu Arg Asp Gly Asp Val Leu Lys Ala Val Ser His Ser Ala His
41 15             20             25             30
43 cac ttt ggg agg gca ata gtc atg cca aat ttg aag cct cct atc act 146
44 His Phe Gly Arg Ala Ile Val Met Pro Asn Leu Lys Pro Pro Ile Thr
45     35             40             45
47 acc act gct gct gct gta gca tac cgg gag gcg ata ttg aaa tct tta 194
48 Thr Thr Ala Ala Ala Val Ala Tyr Arg Glu Ala Ile Leu Lys Ser Leu
49     50             55             60
51 cct gtt gat agt gat ttc aac cct ctt atg aca ctt tat ttg aca gat 242
52 Pro Val Asp Ser Asp Phe Asn Pro Leu Met Thr Leu Tyr Leu Thr Asp
53     65             70             75
55 aca acc agt cct atg gaa atc aaa cta gca aga gag agc cag gtc gta 290
56 Thr Thr Ser Pro Met Glu Ile Lys Leu Ala Arg Glu Ser Gln Val Val
57     80             85             90
59 ttt ggg gtg aag ttg tac cct gct ggt gcc acg aca aat tct caa gat 338
60 Phe Gly Val Lys Leu Tyr Pro Ala Gly Ala Thr Thr Asn Ser Gln Asp
61 95             100             105             110
63 gga gtg act gat ctt ttc ggg aag tgt tta cca gtt cta caa gaa atg 386
64 Gly Val Thr Asp Leu Phe Gly Lys Cys Leu Pro Val Leu Gln Glu Met

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65          115          120          125
67 gtt gag cat aat atg cct ctg ctg gtt cat gga gag gtt act aat cct 434
68 Val Glu His Asn Met Pro Leu Leu Val His Gly Glu Val Thr Asn Pro
69          130          135          140
71 gag gtt gac atg ttt gat aga gaa aag gta ttc att gaa acg gtt cta 482
72 Glu Val Asp Met Phe Asp Arg Glu Lys Val Phe Ile Glu Thr Val Leu
73          145          150          155
75 aga ccg ttg gtg cag aaa ttt cca caa ttg aag gtc gtg atg gag cat 530
76 Arg Pro Leu Val Gln Lys Phe Pro Gln Leu Lys Val Val Met Glu His
77          160          165          170
79 gtt acc acc att gat gct gtt aag ttt gtt gaa tct tgc act gaa gga 578
80 Val Thr Thr Ile Asp Ala Val Lys Phe Val Glu Ser Cys Thr Glu Gly
81 175          180          185          190
83 ttt gtt gca gca act gtc acc cca caa cat ctt gtt ttg aac agg aat 626
84 Phe Val Ala Ala Thr Val Thr Pro Gln His Leu Val Leu Asn Arg Asn
85          195          200          205
87 tct ctc ttc caa ggg ggc tta caa ccg cat aat tac tgc ctt cca gtc 674
88 Ser Leu Phe Gln Gly Gly Leu Gln Pro His Asn Tyr Cys Leu Pro Val
89          210          215          220
91 ctc aaa aga gag atc cac agg gag gca ctt gtg tca gct gta aca agt 722
92 Leu Lys Arg Glu Ile His Arg Glu Ala Leu Val Ser Ala Val Thr Ser
93          225          230          235
95 gga agt aaa aga ttt ttt ctt ggg act gat agt gct cct cat gat aga 770
96 Gly Ser Lys Arg Phe Phe Leu Gly Thr Asp Ser Ala Pro His Asp Arg
97          240          245          250
99 cga aga aaa gag tgt tct tgt gga tgt gct ggt att tac aat gca cct 818
100 Arg Arg Lys Glu Cys Ser Cys Gly Cys Ala Gly Ile Tyr Asn Ala Pro
101 255          260          265          270
103 gta gcc ttg tca gta tat gcg aag gtg ttt gaa aag gaa aat gca ctc 866
104 Val Ala Leu Ser Val Tyr Ala Lys Val Phe Glu Lys Glu Asn Ala Leu
105          275          280          285
107 gac aag ctt gaa gca ttc act agc ttc aat gga cca gat ttt tat ggg 914
108 Asp Lys Leu Glu Ala Phe Thr Ser Phe Asn Gly Pro Asp Phe Tyr Gly
109          290          295          300
111 ctt cct agg aac aac tca aag att aag ttg agt aag acg cca tgg aag 962
112 Leu Pro Arg Asn Asn Ser Lys Ile Lys Leu Ser Lys Thr Pro Trp Lys
113          305          310          315
115 gta ccc gaa tcc ttt tct tat gca tca gga gat att att ccc atg ttt 1010
116 Val Pro Glu Ser Phe Ser Tyr Ala Ser Gly Asp Ile Ile Pro Met Phe
117          320          325          330
119 gct ggt gaa atg ctc gac tgg ttg ccg gct cct ctc tgagaatcat 1056
120 Ala Gly Glu Met Leu Asp Trp Leu Pro Ala Pro Leu
121 335          340          345
123 ttgtcattct tgtactgtaa tattgtgatt caaccaaga tatagactgt aggtgtatca 1116
125 tcttttcttt catgttgatt agatattatc acgatgataa tatectttca gctaataaat 1176
127 tatggaaaca ataagctttg cacgctcacc aaagtgtcc tgtattctga agttcttaaa 1236
129 ttgttcgttt gattttgaag atttactgat aaaaa 1271
133 <210> SEQ ID NO: 2.
134 <211> LENGTH: 346

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135 <212> TYPE: PRT
136 <213> ORGANISM: Solanum tuberosum
138 <400> SEQUENCE: 2
140 Met Glu Leu Ser Ile Thr Gln Pro Asp Asp Trp His Leu His Leu Arg
141   1           5           10           15
143 Asp Gly Asp Val Leu Lys Ala Val Val Ser His Ser Ala His His Phe
144           20           25           30
146 Gly Arg Ala Ile Val Met Pro Asn Leu Lys Pro Pro Ile Thr Thr Thr
147           35           40           45
149 Ala Ala Ala Val Ala Tyr Arg Glu Ala Ile Leu Lys Ser Leu Pro Val
150           50           55           60
152 Asp Ser Asp Phe Asn Pro Leu Met Thr Leu Tyr Leu Thr Asp Thr Thr
153 65           70           75           80
155 Ser Pro Met Glu Ile Lys Leu Ala Arg Glu Ser Gln Val Val Phe Gly
156           85           90           95
158 Val Lys Leu Tyr Pro Ala Gly Ala Thr Thr Asn Ser Gln Asp Gly Val
159           100          105          110
161 Thr Asp Leu Phe Gly Lys Cys Leu Pro Val Leu Gln Glu Met Val Glu
162           115          120          125
164 His Asn Met Pro Leu Leu Val His Gly Glu Val Thr Asn Pro Glu Val
165           130          135          140
167 Asp Met Phe Asp Arg Glu Lys Val Phe Ile Glu Thr Val Leu Arg Pro
168 145          150          155          160
170 Leu Val Gln Lys Phe Pro Gln Leu Lys Val Val Met Glu His Val Thr
171           165          170          175
173 Thr Ile Asp Ala Val Lys Phe Val Glu Ser Cys Thr Glu Gly Phe Val
174           180          185          190
176 Ala Ala Thr Val Thr Pro Gln His Leu Val Leu Asn Arg Asn Ser Leu
177           195          200          205
179 Phe Gln Gly Gly Leu Gln Pro His Asn Tyr Cys Leu Pro Val Leu Lys
180           210          215          220
182 Arg Glu Ile His Arg Glu Ala Leu Val Ser Ala Val Thr Ser Gly Ser
183 225          230          235          240
185 Lys Arg Phe Phe Leu Gly Thr Asp Ser Ala Pro His Asp Arg Arg Arg
186           245          250          255
188 Lys Glu Cys Ser Cys Gly Cys Ala Gly Ile Tyr Asn Ala Pro Val Ala
189           260          265          270
191 Leu Ser Val Tyr Ala Lys Val Phe Glu Lys Glu Asn Ala Leu Asp Lys
192           275          280          285
194 Leu Glu Ala Phe Thr Ser Phe Asn Gly Pro Asp Phe Tyr Gly Leu Pro
195           290          295          300
197 Arg Asn Asn Ser Lys Ile Lys Leu Ser Lys Thr Pro Trp Lys Val Pro
198 305          310          315          320
200 Glu Ser Phe Ser Tyr Ala Ser Gly Asp Ile Ile Pro Met Phe Ala Gly
201           325          330          335
203 Glu Met Leu Asp Trp Leu Pro Ala Pro Leu
204           340          345
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 1962

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208 <212> TYPE: DNA
209 <213> ORGANISM: Nicotiana tabacum
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (305)..(1678)
215 <400> SEQUENCE: 3
217 gaattcggca cgagcacaaa agtagaaagg gttttgctct cccctttcat ctgtgtctca 60
219 taactgtgct aaaacctctc ccattctccc tcaagaacaa agccacccca aaacaccacc 120
221 ttgtacactc ccattgtcgc ttccagtttt gtgccccaaa taaccttttc agtcattttg 180
223 atcttagcat caacaacagt tgctgtctct cttttgttcg tccaatatac tgagcatttt 240
225 ttgagtagta atttgaaggg tttattcagt tgtaaatat ttgatttttg ttttgtttaa 300
227 gaaa atg aga caa agg gtt gga ttt gca ttg att aga gaa agc ttg tat 349
228 Met Arg Gln Arg Val Gly Phe Ala Leu Ile Arg Glu Ser Leu Tyr
229      1      5      10      15
231 cgt aag cta aaa cca agc tct gtt ccc aga cat tat tgc act tct tct 397
232 Arg Lys Leu Lys Pro Ser Ser Val Pro Arg His Tyr Cys Thr Ser Ser
233      20      25      30
235 tca gct aat gtt cct cct att cct cca cct aag att cct cat tct tct 445
236 Ser Ala Asn Val Pro Pro Ile Pro Pro Pro Lys Ile Pro His Ser Ser
237      35      40      45
239 aaa aag gga agg ttg ttt aca gga gcc act att ggt cta cta ata gct 493
240 Lys Lys Gly Arg Leu Phe Thr Gly Ala Thr Ile Gly Leu Leu Ile Ala
241      50      55      60
243 ggg gga gct tat gca agt acg gtt gat gag gcc acc ttc tgt ggc tgg 541
244 Gly Gly Ala Tyr Ala Ser Thr Val Asp Glu Ala Thr Phe Cys Gly Trp
245      65      70      75
247 cta ttc tca gca aca aaa cta gta aat ccg ttc ttt gca ttt ctg gat 589
248 Leu Phe Ser Ala Thr Lys Leu Val Asn Pro Phe Phe Ala Phe Leu Asp
249      80      85      90      95
251 cca gag gtt gct cac aaa ctg gcg gtc tct gct gca gcc cga gga tgg 637
252 Pro Glu Val Ala His Lys Leu Ala Val Ser Ala Ala Ala Arg Gly Trp
253      100     105     110
255 gtt cca agg gag aag agg cca gat cct cct ata ttg ggc ctt gat gtg 685
256 Val Pro Arg Glu Lys Arg Pro Asp Pro Pro Ile Leu Gly Leu Asp Val
257      115     120     125
259 tgg gga aga agg ttc tca aat cct gtt ggt ctt gct gct ggt ttt gac 733
260 Trp Gly Arg Arg Phe Ser Asn Pro Val Gly Leu Ala Ala Gly Phe Asp
261      130     135     140
263 aag aat gct gag gct gtt gaa gga ttg ctt gga tta ggt ttt ggc ttt 781
264 Lys Asn Ala Glu Ala Val Glu Gly Leu Leu Gly Leu Gly Phe Gly Phe
265      145     150     155
267 gtt gag gtt ggc tca gta act ccc att cca cag gaa ggc aac cca aaa 829
268 Val Glu Val Gly Ser Val Thr Pro Ile Pro Gln Glu Gly Asn Pro Lys
269      160     165     170     175
271 cca cgt ata ttt agg ttg cca aat gaa ggt gct ata ata aat agg tgt 877
272 Pro Arg Ile Phe Arg Leu Pro Asn Glu Gly Ala Ile Ile Asn Arg Cys
273      180     185     190
275 ggc ttc aat agt gaa gga atc gtt gtg gtt gcc aaa cga ttg ggt gct 925
276 Gly Phe Asn Ser Glu Gly Ile Val Val Val Ala Lys Arg Leu Gly Ala

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| | | | | | | | | |
|-----|---|------|-----|-----|-----|-----|-----|--|
| 277 | | 195 | | 200 | | 205 | | |
| 279 | cag cat ggt aag aga aag ttg gaa aca tct agt act tca tct cca gct | 973 | | | | | | |
| 280 | Gln His Gly Lys Arg Lys Leu Glu Thr Ser Ser Thr Ser Ser Pro Ala | | | | | | | |
| 281 | | 210 | | 215 | | 220 | | |
| 283 | gga gat gaa gtc aag cat gga ggg aaa gct ggt cct ggt att ctt ggt | 1021 | | | | | | |
| 284 | Gly Asp Glu Val Lys His Gly Gly Lys Ala Gly Pro Gly Ile Leu Gly | | | | | | | |
| 285 | | 225 | | 230 | | 235 | | |
| 287 | gtt aac ctt gga aag aat aaa aca agt gaa gac gct gca gca gat tat | 1069 | | | | | | |
| 288 | Val Asn Leu Gly Lys Asn Lys Thr Ser Glu Asp Ala Ala Ala Asp Tyr | | | | | | | |
| 289 | 240 | | 245 | | 250 | | 255 | |
| 291 | gtg caa gga gtc cat aca tta tct cag tat gct gac tac ttg gta att | 1117 | | | | | | |
| 292 | Val Gln Gly Val His Thr Leu Ser Gln Tyr Ala Asp Tyr Leu Val Ile | | | | | | | |
| 293 | | 260 | | 265 | | 270 | | |
| 295 | aat atc tca tcc cca aat act cca gga cta cgc cag ctt cag gga aga | 1165 | | | | | | |
| 296 | Asn Ile Ser Ser Pro Asn Thr Pro Gly Leu Arg Gln Leu Gln Gly Arg | | | | | | | |
| 297 | | 275 | | 280 | | 285 | | |
| 298 | aag cag ttg aag gat ctt gtg aag aag gtt caa gca gct cgt gat gaa | 1213 | | | | | | |
| 299 | Lys Gln Leu Lys Asp Leu Val Lys Lys Val Gln Ala Ala Arg Asp Glu | | | | | | | |
| 300 | | 290 | | 295 | | 300 | | |
| 302 | atg cag tgg ggt gag gaa gga cct ccg cct tta ctt gtg aaa att gct | 1261 | | | | | | |
| 303 | Met Gln Trp Gly Glu Glu Gly Pro Pro Pro Leu Leu Val Lys Ile Ala | | | | | | | |
| 304 | | 305 | | 310 | | 315 | | |
| 306 | cca gat ttg tct aaa caa gat ctt gaa gat att gca gtg gtg gct gtt | 1309 | | | | | | |
| 307 | Pro Asp Leu Ser Lys Gln Asp Leu Glu Asp Ile Ala Val Val Ala Val | | | | | | | |
| 308 | 320 | | 325 | | 330 | | 335 | |
| 310 | gct ctt cgt gtg gat gga ctg att ata tca aat act act gtc caa aga | 1357 | | | | | | |
| 311 | Ala Leu Arg Val Asp Gly Leu Ile Ile Ser Asn Thr Thr Val Gln Arg | | | | | | | |
| 312 | | 340 | | 345 | | 350 | | |
| 314 | cca gat tcc ata agt caa aac cct gtg gct caa gag gct ggt ggc ttg | 1405 | | | | | | |
| 315 | Pro Asp Ser Ile Ser Gln Asn Pro Val Ala Gln Glu Ala Gly Gly Leu | | | | | | | |
| 316 | | 355 | | 360 | | 365 | | |
| 318 | agt ggg aag cca ctc ttt gac atg tca aca aat ata ctg aag gag atg | 1453 | | | | | | |
| 319 | Ser Gly Lys Pro Leu Phe Asp Met Ser Thr Asn Ile Leu Lys Glu Met | | | | | | | |
| 320 | | 370 | | 375 | | 380 | | |
| 322 | tac gtt ctg act aag gga agg att cct ctg att ggc act ggg ggt att | 1501 | | | | | | |
| 323 | Tyr Val Leu Thr Lys Gly Arg Ile Pro Leu Ile Gly Thr Gly Gly Ile | | | | | | | |
| 324 | | 385 | | 390 | | 395 | | |
| 326 | agc agt ggc gag gat gct tac aag aaa att cga gct ggt gcc act ctt | 1549 | | | | | | |
| 327 | Ser Ser Gly Glu Asp Ala Tyr Lys Lys Ile Arg Ala Gly Ala Thr Leu | | | | | | | |
| 328 | 400 | | 405 | | 410 | | 415 | |
| 330 | gtt cag ctt tat aca gca ttt gca tat gga ggc cct gca ctt atc ccc | 1597 | | | | | | |
| 331 | Val Gln Leu Tyr Thr Ala Phe Ala Tyr Gly Gly Pro Ala Leu Ile Pro | | | | | | | |
| 332 | | 420 | | 425 | | 430 | | |
| 334 | gat ata aag gat gaa ctt gct cgt tgc tta gaa aag gat ggt tat aag | 1645 | | | | | | |
| 335 | Asp Ile Lys Asp Glu Leu Ala Arg Cys Leu Glu Lys Asp Gly Tyr Lys | | | | | | | |
| 336 | | 435 | | 440 | | 445 | | |
| 338 | tca atc agt gag gct gtt gga gca gac tgc aga tagtagtagt tgatatacta | 1698 | | | | | | |
| 339 | Ser Ile Ser Glu Ala Val Gly Ala Asp Cys Arg | | | | | | | |
| 340 | | 450 | | 455 | | | | |

VERIFICATION SUMMARY

DATE: 08/02/2005

PATENT APPLICATION: US/10/070,277A

TIME: 15:48:59

Input Set : N:\KEISHA\10070277A.txt

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